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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/846,658B*

164

DATE: 08/18/98
TIME: 09:57:42

INPUT SET: S28075.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING **ENTERED**

```
1                                    SEQUENCE LISTING
2
3    (1)    General Information:
4
5      (i)  APPLICANT: Adair, John R.
6                     Athwal, Diljeet S.
7                     Emtage, John S.
8
9     (ii)       TITLE OF INVENTION: Humanised Antibodies
10
11   (iii)       NUMBER OF  SEQUENCES: 30 .
12
13    (iv)       CORRESPONDENCE  ADDRESS:
14         (A)   ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
15         (B)   STREET: One Liberty Place - 46th Floor
16         (C)   CITY:   Philadelphia
17         (D)   STATE: PA
18         (E)   COUNTRY: USA
19         (F)   ZIP: 19103
20
21    (v)  COMPUTER  READABLE  FORM:
22         (A)   MEDIUM TYPE: Floppy disk
23         (B)   COMPUTER: IBM PC compatible
24         (C)   OPERATING SYSTEM: PC-DOS/MS-DOS
25         (D)   SOFTWARE: PatentIn Release #1.0, Version #1.25
26
27    (vi)       CURRENT APPLICATION DATA:
28         (A)   APPLICATION NUMBER: US 08/846,658
29         (B)   FILING DATE: 01-MAY-1997
30         (C)   CLASSIFICATION:
31
32    (viii)     ATTORNEY/AGENT INFORMATION:
33         (A)   NAME: Trujillo, Doreen Yatko
34         (B)   REGISTRATION NUMBER: 35,719
35         (C)   REFERENCE/DOCKET NUMBER: CARP-0057
36
37    (ix)       TELECOMMUNICATION INFORMATION:
38         (A)   TELEPHONE: (215) 568-3100
39         (B)   TELEFAX: (215) 568-3439
40
41
42   (2) INFORMATION FOR SEQ ID NO:1:
43
44     (i) SEQUENCE CHARACTERISTICS:
45         (A) LENGTH: 20 base pairs
46         (B) TYPE: nucleic  acid
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47              (C) STRANDEDNESS: single
48              (D) TOPOLOGY: linear
49
50        (ii) MOLECULE TYPE: cDNA
51
52
53        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
54
55   TCCAGATGTT AACTGCTCAC                                    20
56
57   (2) INFORMATION FOR SEQ ID NO:2:
58
59        (i) SEQUENCE CHARACTERISTICS:
60              (A) LENGTH: 23 base pairs
61              (B) TYPE: nucleic acid
62              (C) STRANDEDNESS:  single
63              (D) TOPOLOGY:  linear
64
65        (ii) MOLECULE TYPE: cDNA
66
67
68
69        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
70
71   CAGGGGCCAG TGGATGGATA GAC                                23
72
73   (2) INFORMATION FOR SEQ ID NO:3:
74
75        (i) SEQUENCE CHARACTERISTICS:
76              (A) LENGTH: 9 amino acids
77              (B) TYPE: amino  acid
78              (C) STRANDEDNESS:  single
79              (D) TOPOLOGY:  linear
80
81        (ii) MOLECULE TYPE: peptide
82
83
84
85        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
86
87   Leu Glu Ile Asn Arg Thr Val Ala Ala
88   1                 5
89
90   (2) INFORMATION FOR SEQ ID NO:4:
91
92        (i) SEQUENCE CHARACTERISTICS:
93              (A) LENGTH: 943 base pairs
94              (B) TYPE: nucleic acid
95              (C) STRANDEDNESS:  single
96              (D) TOPOLOGY:  linear
97
98        (ii) MOLECULE TYPE: cDNA
99
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100
101          (ix) FEATURE:
102              (A) NAME/KEY: CDS
103              (B) LOCATION: 18..722
104
105          (ix) FEATURE:
106              (A) NAME/KEY: mat_peptide
107              (B) LOCATION: 84..722
108
109
110          (xi) SEQUENCE DESCRIPTION: SEQ  ID  NO:4:
111
112    GAATTCCCAA AGACAAA ATG GAT TTT CAA GTG CAG ATT TTC AGC TTC CTG        50
113                        Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu
114                        -22      -20                     -15

115
116    CTA ATC AGT GCC TCA GTC ATA ATA TCC AGA GGA CAA ATT GTT CTC ACC        98
117    Leu Ile Ser Ala Ser Val Ile Ile Ser Arg Gly Gln Ile Val Leu Thr
118    -10                 -5                   1                   5
119
120    CAG TCT CCA GCA ATC ATG TCT GCA TCT CCA GGG GAG AAG GTC ACC ATG       146
121    Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met
122                10              15                  20
123
124    ACC TGC AGT GCC AGC TCA AGT GTA AGT TAC ATG AAC TGG TAC CAG CAG       194
125    Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln
126                25                  30                  35
127
128    AAG TCA GGC ACC TCC CCC AAA AGA TGG ATT TAT GAC ACA TCC AAA CTG       242
129    Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu
130                40                  45                  50
131
132    GCT TCT GGA GTC CCT GCT CAC TTC AGG GGC AGT GGG TCT GGG ACC TCT       290
133    Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser
134        55                  60                  65
135
136    TAC TCT CTC ACA ATC AGC GGC ATG GAG GCT GAA GAT GCT GCC ACT TAT       338
137    Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr
138    70                  75                  80                  85
139
140    TAC TGC CAG CAG TGG AGT AGT AAC CCA TTC ACG TTC GGC TCG GGG ACA       386
141    Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr
142                90                  95                  100
143
144    AAG TTG GAA ATA AAC CGG GCT GAT ACT GCA CCA ACT GTA TCC ATC TTC       434
145    Lys Leu Glu Ile Asn Arg Ala Asp Thr Ala Pro Thr Val Ser Ile Phe
146                105                 110                 115
147
148    CCA CCA TCC AGT GAG CAG TTA ACA TCT GGA GGT GCC TCA GTC GTG TGC       482
149    Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys
150                120                 125                 130
151
152    TTC TTG AAC AAC TTC TAC CCC AAA GAC ATC AAT GTC AAG TGG AAG ATT       530
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153   Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile
154       135             140             145

155
156
157   GAT GGC AGT GAA CGA CAA AAT GGC GTC CTG AAC AGT TGG ACT GAT CAG          578
158   Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln
159   150             155             160             165

160
161   GAC AGC AAA GAC AGC ACC TAC AGC ATG AGC AGC ACC CTC ACG TTG ACC          626
162   Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr
163           170             175             180

164
165   AAG GAC GAG TAT GAA CGA CAT AAC AGC TAT ACC TGT GAG GCC ACT CAC          674
166   Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His
167           185             190             195

168
169   AAG ACA TCA ACT TCA CCC ATT GTC AAG AGC TTC AAC AGG AAT GAG TGT          722
170   Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
171           200             205             210

172
173   TAGAGACAAA GGTCCTGAGA CGCCACCACC AGCTCCCAGC TCCATCCTAT CTTCCCTTCT          782

174
175   AAGGTCTTGG AGGCTTCCCC ACAAGCGCTT ACCACTGTTG CGGTGCTCTA AACCTCCTCC          842

176
177   CACCTCCTTC TCCTCCTCCT CCCTTTCCTT GGCTTTTATC ATGCTAATAT TTGCAGAAAA          902

178
179   TATTCAATAA AGTGAGTCTT TGCCTTGAAA AAAAAAAAAA A                            943

180
181
182   (2) INFORMATION FOR SEQ ID NO:5:

183
184           (i) SEQUENCE CHARACTERISTICS:
185                   (A) LENGTH: 235 amino acids
186                   (B) TYPE: amino acid
187                   (D) TOPOLOGY: linear

188
189           (ii) MOLECULE TYPE: protein

190
191           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

192
193   Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
194   -22     -20             -15             -10

195
196   Val Ile Ile Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile
197       -5              1               5               10

198
199   Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser
200               15              20              25

201
202   Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser
203           30              35              40

204
205   Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro
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INPUT SET: S28075.raw

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206              45                      50                      55
207
208   Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
209        60                      65                      70
210
211   Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
212    75                      80                      85                  90
213
214
215   Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn
216                    95                     100                     105
217
218   Arg Ala Asp Thr Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
219                   110                     115                     120
220
221   Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
222             125                     130                     135
223
224   Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
225        140                     145                     150
226
227   Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
228    155                     160                     165                     170
229
230   Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
231                   175                     180                     185
232
233   Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
234             190                     195                     200
235
236   Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
237        205                     210
238
239   (2) INFORMATION FOR SEQ ID NO:6:
240
241       (i) SEQUENCE CHARACTERISTICS:
242           (A) LENGTH: 1570 base pairs
243           (B) TYPE: nucleic  acid
244           (C) STRANDEDNESS: single
245           (D) TOPOLOGY: linear
246
247      (ii) MOLECULE TYPE:  cDNA
248
249
250       (ix) FEATURE:
251           (A) NAME/KEY:  CDS
252           (B) LOCATION:  41..1444
253
254       (ix) FEATURE:
255               (A) NAME/KEY:  mat_peptide
256               (B) LOCATION:  98..1444
257
258
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/846,658B*

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TIME: 09:57:47

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